re-rus)

RAW SEQUENCE LISTING DATE: 03/23/2001
PATENT APPLICATION: US/09/435,770 TIME: 16:39:39

Input Set : A:\Yamamtol.app

Output Set: N:\CRF3\03232001\I435770.raw

Does Not Comply
Corrected Diskette Needed

pp 1-15

FUKUDA, Shigeharu

MIYAKE, TOShio

10 <120> TITLE OF INVENTION: NON-REDUCING SACCHARIDE-FORMING ENZYME,

TREHALOSE-RELEASING ENZYME, AND PROCESS FOR PRODUCING

SACCHARIDES USING THE ENZYMES

14 <130> FILE REFERENCE: YAMAMOTO=16A

16 <140> CURRENT APPLICATION NUMBER: 09/435,770

17 <141> CURRENT FILING DATE: 1999-11-08

19 <150> PRIOR APPLICATION NUMBER: JP 258,394/1998

20 <151> PRIOR FILING DATE: 1998-09-11

22 <150> PRIOR APPLICATION NUMBER: JP 352,252/1998

26 <151> PRIOR FILING DATE: 1999-01-26 28 <160> NUMBER OF SEQ ID NOS: 39 30 <170> SOFTWARE: Patentin Ver. 2.1

23 <151> PRIOR FILING DATE: 1998-12-11

25 <150> PRIOR APPLICATION NUMBER: JP 16,931/1999

4 <110> APPLICANT: YAMAMOTO, Takuo 5 MARUTA, Kazuhiko 6 KUBOTA, Michio

ERRORED SEQUENCES

241 <210> SEQ ID NO: 7 242 <211> LENGTH: 2268

243 <212> TYPE: DNA

244 <213> ORGANISM: ARTHROBACTER sp.S34

246 <400> SEQUENCE: 7

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E--> 249 atogtgccct acctgcaccg cctcggcgcc gactggctgt acctctcgcc gctgctcgag 250 120

E--> 251 teegagtegg geteetegea eggetaegae gtggtegaee acteeegegt egaegeegee 252 180

E--> 253 cgcggcggc cggagggct cgccgagctc tcccgtgcgg cgcacgagcg cggcatgggc 254 240

E--> 255 gtcgtcgtcg acatcgtgcc caaccacgtc ggcgtcgcga cgccgaaggc gaaccgctgg 256 300

E--> 257 tggtgggacg ttctggcccg tggacagcgg tcggagtacg ccgactactt cgacatcgac 258 360

E--> 259 tgggagtteg geggeggeag getgegeetg eeegtgeteg gegaeggeee egaegagete 260 420

E--> 261 gacgcgctga gagtggatgg cgacgagctc gtctactacg agcaccgctt cccgatcgcc 262 480

E--> 263 gagggcaccg gcggcggcac cccgcgcgag gtgcacgacc ggcagcacta cgagctgatg 264 540

E--> 265 tegtggegge gggeegacea egaceteaae tacegeeget tettegeegt gaacaegete

global format enor (see item I on Ever Summary Sheet)

Input Set : A:\Yamamtol.app

266 600

314 2040

Output Set: N:\CRF3\03232001\1435770.raw

E--> 267 geogeogtac gegtegaaga eeegegegtg ttegaegaca eecacegega gateggeege 268 660 E--> 269 tggategeeg agggeetegt egacggeetg egegtegace acceegacgg getgegegee 270 720 E--> 271 cccggcgact acctgcgccg tctcgccgag ctcgcccaag gcaggccgat ctgggtcgag 272 780 E--> 273 aagatcatcg agggcgacga gcggatgccc ccgcagtggc ccatcgccgg caccaccggc 274 840 E--> 275 tacgacgogo tggcogggat ogacogggtg otogtogaco cogogggoga gcatoogoto E--> 277 acccagateg tegaegagge ggeaggeage ecceggeget gggeegaget ggtteeegag 278 960 E--> 279 cgcaageggg cegtegeeeg eggcateetg aacteegaga teegeegegt egeeegegaa 280 1020 E--> 281 ctcggagagg tcgccggcga cgtcgaagac gcgctcgtcg agatcgccgc cgccctgtcc 282 1080 E--> 283 gtctaccgca gctacctgcc gttcgggcgc gagcacctcg acgaagccgt ggccgccgcg 284 1140 E--> 285 caggoogcag coccocaget cgaggoogac etcgcogcog toggogcage getogcogae 286 1200 E--> 287 ccgggcaacc ccgccgcgct ccgcttccag cagaccagcg gcatgatcat ggccaagggc 288 1260 E--> 289 gtcgaggaca acgcgttcta ccgctaccc cggctcacct cgctgaccga ggtcggggga 290 1320 E--> 291 gaccegagee tgttegegat egacgeggee geetteeaeg eggegeageg egacegegee 292 1380 E--> 293 geoeggetge eegagtegat gacgaegetg accaeceaeg acaecaageg eagegaagae 294 1440 E--> 295 acceggege ggateacege getegeegag geceegaac getggeggeg etteetgace 296 1500 E--> 297 gaggtcggcg ggctcatcgg aacgggcgac cgggtgctgg agaacctgat ctggcaggcg 298 1560 E--> 299 atogtoggog cgtggccggc gagccgggag cggctcgagg cctacgcgct gaaggccgcg 300 1620 E--> 301 egegaageeg gegagtegae egaetggate gaeggegaee eegegttega agageggetg 302 1680 E--> 303 accepactg teacggtege egtegaggag cegategtge acgagetget egageggete 304 1740 E--> 305 gtcgacgage tgacggcggc cgggtactec aacggcctcg cggcgaaget gctgcagctg 306 1800 E--> 307 ctegececeg gaacececga egtgtaceag ggcaeggaac getgggaeeg gtegetggtg 308 1860 E--> 309 gacceggaca accetegece egtegattte geogegeat eegageteet egacegeete 310 1920 E--> 311 gacggcggct ggcggccgcc cgtcgacgag accggcgcgg tcaagacgct cgtcgtctcc 312 1980 E--> 313 egegegetge ggetgegeeg egaceggeee gagetgttea eegegtacea eeeggteaeg

son

Input Set : A:\Yamamtol.app

Output Set: N:\CRF3\03232001\I435770.raw E--> 315 gegegeggeg egeaggeega geacetgate ggettegace geggeggege gategeeetg 316 2100 E--> 317 gecaecegee tgeegetegg cetegeegee geaggegget ggggegaeae ggtegtegae 318 2160 E--> 319 qtcggcgagc ggagcctgcg cgacgagctg accggccgcg aggcccgcgg agcggcgcgc 320 2220 E--> 321 gtggccgagt tgttcgccga ctaccccgtc gccctgctgg tggagaca 322 2268 325 <210> SEQ ID NO: 8 326 <211> LENGTH: 28 327 <212> TYPE: DNA 328 <213> ORGANISM: ARTHROBACTER sp.S34 330 <400> SEQUENCE: 8 E--> 331 ttttttaata aaatcaggag gaaaaaat 332 28 529 <210> SEQ ID NO: 17 530 <211> LENGTH: 1725 531 <212> TYPE: DNA 532 <213> ORGANISM: ARTHROBACTER sp.S34 534 <400> SEQUENCE: 17 E--> 535 atgaaccgac gattcccggt ctgggcgccc caggccgcgc aggtgacgct cgtcgtgggc 536 60 E--> 537 caaggeegeg eegaacteee getgaeeege gaegagaaeg gatggtggge tetteageag 538 120 E--> 539 ccgtgggacg gcggccccga cctcgtcgac tacggctacc tcgtcgacgg caagggcccc 540 180 E--> 541 ttcgccgacc cgcggtcgct gcggcagccg cgcggcgtgc acgagctcgg ccgcgaattc

same

- 542 240
 E--> 543 gaccegece getacgegtg gggegacgae ggatggegeg geegagacet caceggagee
- 544 300
 E--> 545 gtgatctacg aactgcacgt cggcaccttc accectgagg gaacgctgga cagegccate
- 546 360
- E--> 547 cgtcgcctcg accacctggt gcgcctcggc gtcgacgcgg tcgagctgct gcccgtcaac 548 420
- E--> 549 gegttcaacg gcacccacgg etggggctac gacggggtgc tetggtacgc ggtgcacgag 550 480
- E--> 551 ccctacggcg gcccggaggc gtaccagcgc ttcgtcgacg cctgccacgc ccgcggcctc 552 540
- E--> 553 gccgtcgtgc aggacgtcgt ctacaaccac ctgggcccga gcggcaacca cctgcccgac 554 600
 E--> 555 ttcggcccct acctcgggtc gggcgccgc aacacctggg gcgacgcgt gaacctcgac
- 556 660 E--> 557 gggccgctct ccgacgaggt gcggcggtac atcatcgaca acgcggtgta ctggctgcgc
- 558 720 E--> 559 gacatgcaeg cegaegget geggetegae geegtgeaeg egetgegega egeeegegeg
- 560 780
 E--> 561 ctgcacctgc tcgaagagct cgccgcccgc gtcgacgagc tggcgggcga gctcggccgg
 562 840
- E--> 563 ccgctgacgc tcatcgccga gagcgacctg aacgacccga agctgatccg ctcccgcgcg

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E--> 565 gcgcacggct acggcctcga cgcccagtgg gacgacgacg tgcaccacgc ggtgcacgcc
     566 960
E--> 567 aacgtgaccg gcgagaccgt cggctactac gccgacttcg gcgggctcgg cgccctcgtc
     568 1020
E--> 569 aaggtgttcc agcgcggctg gttccacgac ggcacctggt cgagcttccg cgagcgcac
     570 1080
E--> 571 cacggccggc cgctcgaccc cgacatcccg ttccgccggc tcgtcgcctt cgcgcaggat
     572 1140
E--> 573 cacgaccagg teggeaaccg ageggtegge gaccgcatgt eggegeaggt eggegagggt
     574 1200
E--> 575 tegetegeeg eegeggegge getegtgetg eteggeeegt teacecegat getgtteatg
     576 1260
E--> 577 ggcgaggagt ggggcgcgcg caccccgtgg cagttcttca cctcccaccc cgagcccgag
     578 1320
E--> 579 ctgggggagg cgacggcgcg cgggcgcatc gccgagttcg cccgcatggg ctgggacccg
     580 1380
E--> 581 gcagtcgtgc ccgacccgca ggacccggcc accttcgccc gctcgcacct ggactggtcc
     582 1440
E--> 583 gagcccgage gggaaccgca cgcgggcctg ctcgccttct acaccgacct gatcgcgctg
     584 1500
E--> 585 cggcgcgagc tgccggtcga tgcgccggcg cgcgaggtgg atgccgacga ggcgcgcggc
     586 1560
E--> 587 gtettegegt teageegegg eeegetgegg gteaeggteg egetgegeee eggaeeggte
     588 1620
E--> 589 ggggtgcccg agcacggggg cctcgtgctc gcctacggcg aggtgcgcgc cggcgccgcc
     590 1680
E--> 591 ggactgcacc tcgacgggcc gggagccgcg atcgtgcgcc tcgag
     592 1725
     595 <210> SEQ ID NO: 18
     596 <211> LENGTH: 23
     597 <212> TYPE: DNA
     598 <213> ORGANISM: ARTHROBACTER sp.S34
     600 <400> SEQUENCE: 18
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     602 23
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     606 <211> LENGTH: 3252
     607 <212> TYPE: DNA
     608 <213> ORGANISM: ARTHROBACTER sp.S34
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     612 <222> LOCATION: (1)..(742)
    614 <220> FEATURE:
     615 <221> NAME/KEY: CDS
     616 <222> LOCATION: (743)..(3013)
    618 <220> FEATURE:
    619 <221> NAME/KEY: 3'UTR
    620 <222> LOCATION: (742)..(3014)
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Some

Input Set : A:\Yamamtol.app

Output Set: N:\CRF3\03232001\I435770.raw

622 <400> SEQUENCE: 19 E--> 623 atgccgacga cgaacttgag cgcgttctcg ggcacccgcg agagcggtcc gcgcacggcg 624 60 E--> 626 gcgcccagtg ccacgacgag cacgatcgcg gcgagcgccg cgacgacggc gaccggcagg 627 120 E--> 629 cgccctgat tgctggcgaa ggtgagcacg atgaagacca cctcgaggcc ctcgagcaac 630 180 E--> 632 acacettiga acgacacggt gaacgcgtac caateggaga eccegaaceg getetegege 633 240 E--> 635 cgggcgctct cggccgcctc gacctgacgc cggaaggcag cctcctcgtc acggagagcc 636 300 E--> 638 ctgcgccctg ccgcgcgcag caccgccttg cgcagccagc cgagcccgaa gacgagcagc E--> 641 aacccgccga cgacgaggcg cagcacggcc agcggcagca gcaggatcgc gggaccgacg 642 420 E--> 644 agegegacgg cegeggecag caccaccacg gegacggegg cacctgtcag egeegacege 645 480 E--> 647 cagetgeggg tggegeegae egegaegaeg ategtggteg eeteeaeege etegaeeaeg 648 540 E--> 650 caggcgagga acacggcggc gaacagggcg acggcggtca tcggcccagc agacggttga 651 600 E--> 653 ccatcacggc acgctagcgc cattgctcac aggaagggcc aagacgcccg caacgcggca 654 660 E--> 656 cccgtggacg gcgcgtaccg gcgtgtgacc gatcgtgtca accggtggcg cccgccccga 657 720 E--> 659 gcacctgcgt agattcggcc tc gtg ccc gcc agt acc tac cgc ctt cag atc 660 772 661 Met Pro Ala Ser Thr Tyr Arg Leu Gln Ile 662 1 5 E--> 664 tog gog gag tto acc etc tto gac gog gog egc atc gtg ccc tac etg 665 820 666 Ser Ala Glu Phe Thr Leu Phe Asp Ala Ala Arg Ile Val Pro Tyr Leu 667 15 20 E--> 669 cac egc etc gge gee gae tgg etg tac etc teg eeg etg etc gag tee 670 868 671 His Arg Leu Gly Ala Asp Trp Leu Tyr Leu Ser Pro Leu Leu Glu Ser 672 30 35 E--> 674 gag tog ggo too tog cao ggo tao gao gtg gto gao cao too ogo gto 675 916 676 Glu Ser Gly Ser Ser His Gly Tyr Asp Val Val Asp His Ser Arg Val 677 45 50 E--> 679 gac gcc gcc cgc ggc ggg ccg gag ggg ctc gcc gag ctc tcc cgt gcg 680 964 681 Asp Ala Ala Arg Gly Gly Pro Glu Gly Leu Ala Glu Leu Ser Arg Ala 682 60 65 70 E--> 684 gcg cac gag cgc ggc atg ggc gtc gtc gtc gac atc gtg ccc aac cac 685 1012 686 Ala His Glu Arg Gly Met Gly Val Val Val Asp Ile Val Pro Asn His 687 75 80 85

pare

Input Set : A:\Yamamto1.app
Output Set: N:\CRF3\03232001\I435770.raw

E--> 689 gtc ggc gtc gcg acg ccg aag gcg aac cgc tgg tgg tgg gac gtt ctg 690 1060 691 Val Gly Val Ala Thr Pro Lys Ala Asn Arg Trp Trp Trp Asp Val Leu 692 95 100 E--> 694 gcc cgt gga cag cgg tcg gag tac gcc gac tac ttc gac atc gac tgg 695 1108 696 Ala Arg Gly Gln Arg Ser Glu Tyr Ala Asp Tyr Phe Asp Ile Asp Trp 697 110 115 E--> 699 gag ttc ggc ggc ggc agg ctg cgc ctg ccc gtg ctc ggc gac ggc ccc 700 1156 701 Glu Phe Gly Gly Gly Arg Leu Arg Leu Pro Val Leu Gly Asp Gly Pro 702 125 130 135 E--> 704 gac gag ctc gac gcg ctg aga gtg gat ggc gac gag ctc gtc tac tac 705 1204 706 Asp Glu Leu Asp Ala Leu Arg Val Asp Gly Asp Glu Leu Val Tyr Tyr 707 140 145 E--> 709 gag cac ege tte eeg ate gee gag gge ace gge gge ace eeg ege 710 1252 711 Glu His Arg Phe Pro Ile Ala Glu Gly Thr Gly Gly Gly Thr Pro Arg 712 155 160 165 E--> 714 gag gtg cac gac cgg cag cac tac gag ctg atg tcg tgg cgg cgc 715 1300 716 Glu Val His Asp Arg Gln His Tyr Glu Leu Met Ser Trp Arg Arg Ala 175 180 717 185 E--> 719 gac cac gac ctc aac tac cgc cgc ttc ttc gcc gtg aac acg ctc gcc 721 Asp His Asp Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu Ala 722 190 195 E--> 724 gcc gta cgc gtc gaa gac ccg cgc gtg ttc gac gac acc cac cgc gag 725 1396 726 Ala Val Arg Val Glu Asp Pro Arg Val Phe Asp Asp Thr His Arg Glu

210

731 Ile Gly Arg Trp Ile Ala Glu Gly Leu Val Asp Gly Leu Arg Val Asp

736 His Pro Asp Gly Leu Arg Ala Pro Gly Asp Tyr Leu Arg Arg Leu Ala

741 Glu Leu Ala Gln Gly Arg Pro Ile Trp Val Glu Lys Ile Ile Glu Gly

746 Asp Glu Arg Met Pro Pro Gln Trp Pro Ile Ala Gly Thr Thr Gly Tyr

260

275

E--> 729 atc ggc cgc tgg atc gcc gag ggc ctc gtc gac ggc ctg cgc gtc gac

E--> 734 cac ccc gac ggg ctg cgc gcc ccc ggc gac tac ctg cgc cgt ctc gcc

E--> 739 gag ctc gcc caa ggc agg ccg atc tgg gtc gag aag atc atc gag ggc

E--> 744 gac gag cgg atg ccc ccg cag tgg ccc atc gcc ggc acc acc ggc tac

E--> 749 gac gcg ctg gcc ggg atc gac cgg gtg ctc gtc gac ccc gcg ggc gag

225

240

255

270

215

265

230

245

Same

727

730 1444

735 1492

737 235

740 1540

745 1588

742

747

732 220

205

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/435,770

DATE: 03/23/2001 TIME: 16:39:39

Input Set : A:\Yamamtol.app

Output Set: N:\CRF3\03232001\1435770.raw

750 1636 751 Asp Ala Leu Ala Gly Ile Asp Arg Val Leu Val Asp Pro Ala Gly Glu 752 285 290 295 E--> 754 cat ccg ctc acc cag atc gtc gac gag gcg gca ggc agc ccc cgg cgc 755 1684 756 His Pro Leu Thr Gln Ile Val Asp Glu Ala Ala Gly Ser Pro Arg Arg 305 310 E--> 759 tgg gcc gag ctg gtt ccc gag cgc aag cgg gcc gtc gcc cgc ggc atc 760 1732 761 Trp Ala Glu Leu Val Pro Glu Arg Lys Arg Ala Val Ala Arg Gly Ile 762 315 320 325 E--> 764 ctg aac tcc gag atc cgc cgc gtc gcc cgc gaa ctc gga gag gtc gcc 765 1780 766 Leu Asn Ser Glu Ile Arg Arg Val Ala Arg Glu Leu Gly Glu Val Ala 340 335 E--> 769 ggc gac gtc gaa gac gcg ctc gtc gag atc gcc gcc gcc ctg tcc gtc 770 1828 771 Gly Asp Val Glu Asp Ala Leu Val Glu Ile Ala Ala Ala Leu Ser Val 772 350 355 E--> 774 tac cgc agc tac ctg ccg ttc ggg cgc gag cac ctc gac gaa gcc gtg 775 1876 776 Tyr Arg Ser Tyr Leu Pro Phe Gly Arg Glu His Leu Asp Glu Ala Val 777 365 370 375 E--> 779 gcc gcc gcg cag gcc gca gcc ccc cag ctc gag gcc gac ctc gcc gcc 780 1924 781 Ala Ala Ala Gln Ala Ala Ala Pro Gln Leu Glu Ala Asp Leu Ala Ala 782 380 385 390 E--> 784 gtc ggc gca gcg ctc gcc gac ccg ggc aac ccc gcc gcg ctc cgc ttc 785 1972 786 Val Gly Ala Ala Leu Ala Asp Pro Gly Asn Pro Ala Ala Leu Arg Phe 787 395 400 E--> 789 cag cag acc agc ggc atg atc atg gcc aag ggc gtc gag gac aac gcg 790 2020 791 Gln Gln Thr Ser Gly Met Ile Met Ala Lys Gly Val Glu Asp Asn Ala 792 415 E--> 794 ttc tac ege tac eec egg etc ace teg etg ace gag gtc ggg gga gac 795 2068 796 Phe Tyr Arg Tyr Pro Arg Leu Thr Ser Leu Thr Glu Val Gly Gly Asp 797 430 435 E--> 799 ccg agc ctg ttc gcg atc gac gcg gcc ttc cac gcg gcg cag cgc 800 2116 801 Pro Ser Leu Phe Ala Ile Asp Ala Ala Ala Phe His Ala Ala Gln Arg 802 445 450 E--> 804 gac ege gee egg etg eec gag teg atg acg acg etg acc acc eac 805 2164 806 Asp Arg Ala Ala Arg Leu Pro Glu Ser Met Thr Thr Leu Thr Thr His 807 460 465 E--> 809 gac acc aag cgc agc gaa gac acc cgg gcg cgg atc acc gcg ctc gcc

some

810 2212

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/435,770 DATE: 03/23/2001 TIME: 16:39:39

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Output Set: N:\CRF3\03232001\I435770.raw

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		Glu Ala	Pro	Glu	Arg	Trp	Arg	Arg	Phe	Leu	Thr	Glu	Val	Gly	Gly	Leu
_	817				495					500					505	
E>		atc gga 2308	acg	ggc	gac	cgg	gtg	ctg	gag	aac	ctg	atc	tgg	cag	gcg	atc
		Ile Gly	Thr	Gly	Asp	Arg	Val	Leu	Glu	Asn	Leu	Ile	Trp	Gln	Ala	Ile
	822			510					515					520		
E>		gtc ggc 2356	gcg	Egg	ccg	gcg	agc	cgg	gag	cgg	CTC	gag	gcc	tac	gcg	ctg
		Val Gly		Trp	Pro	Ala	ser		Glu	Arg	Leu	Glu		Tyr	Ala	Leu
	827		525					530				.	535			
E>		aag gcc 2404	gcg	cgc	gaa	gee	ggc	gag	ceg	acc	gac	cgg	acc	gac	gge	gac
	831	Lys Ala	Ala	Arg	Glu	Ala	Gly	Glu	Ser	Thr	Asp	Trp	Ile	Asp	Gly	Asp
	832	540					545					550				
E>		ccc gcg 2452	ttc	gaa	gag	cgg	ctg	acc	cgc	ctg	gtc	acg	gtc	gcc	gtc	gag
	_	Pro Ala	Phe	Glu	Glu	Arg	Leu	Thr	Arg	Leu	Val	Thr	Val	Ala	Val	Glu
		555				560	_				565					570
E>		gag ccg 2500	ctc	gtg	cac	gag	ctg	ctc	gag	cgg	ctc	gtc	gac	gag	ctg	acg
		Glu Pro	Leu	Val	His	Glu	Leu	Leu	Glu	Arg	Leu	Val	Asp	Glu	Leu	Thr
	842				575					580					585	
E>		gcg gcc 2548	ggg	tac	tcc	aac	ggc	ctc	gcg	gcg	aag	ctg	ctg	cag	ctg	ctc
	-	Ala Ala	Gly	Tyr	Ser	Asn	Gly	Leu	Ala	Ala	Lys	Leu	Leu	Gln	Leu	Leu
	847			590					595					600		
E>		gcc ccc 2596	gga	acc	ccc	gac	gtg	tac	cag	ggc	acg	gaa	cgc	tgg	gac	cgg
		Ala Pro	Glv	Thr	Pro	Asp	Val	Tyr	Gln	Glv	Thr	Glu	Arq	Trp	Asp	Arq
	852		605					610					615			
E>		tcg ctg	gtg	gac	ccg	gac	aac	cgt	cgc	ccc	gtg	gat	ttc	gcc	gcg	gca
		2644 Ser Leu	Val	Asn	Pro	Asn	Asn	Ara	Ara	Pro	Val	Asn	Phe	Ala	Ala	Ala
	857	620					625		5			630				
E>		tcc gag 2692	ctg	ctc	gac	cgc	ctc	gac	ggc	ggc	tgg	cgg	ccg	ccc	gtc	gac
		Ser Glu	Leu	Leu	Asp	Ara	Leu	Asp	Glv	Glv	Trp	Arq	Pro	Pro	Val	Asp
		635				640			1	1	645					650
E>		gag acc	ggc	gcg	gtc	aag	acg	ctc	gtc	gtc	tcc	cgc	gcg	ctg	cgg	ctg
		2740 Glu Thr	Glv	Ala	Val	Lvs	Thr	Leu	Va 1	Va l	Ser	Ara	Ala	Leu	Ara	Leu
	867		_		655	_				660		_			665	
E>		cgc cgc	gac	cgg	ccc	gag	ctg	ttc	acc	gcg	tac	cac	ccg	gtc	acg	gcg
		2788 Arg Arg	Agn	Arg	Pro	Glu	Len	Phe	Thr	Ala	Tvr	His	Pro	Val	Thr	Ala
	3,1	y niy		9	-10	JIU	LCu		1111		-1-					

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Input Set : A:\Yamamtol.app

Output Set: N:\CRF3\03232001\I435770.raw

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E--> 874 cgc ggc gcg cag gcc gag cac ctg atc ggc ttc gac cgc ggc gcg
     875 2836
     876 Arg Gly Ala Gln Ala Glu His Leu Ile Gly Phe Asp Arg Gly Gly Ala
                685
                                     690
                                                         695
E--> 879 atc gcc ctg gcc acc cgc ctg ccg ctc ggc ctc gcc gcc gca ggc ggc
     880 2884
     881 Ile Ala Leu Ala Thr Arg Leu Pro Leu Gly Leu Ala Ala Ala Gly Gly
     882
            700
                                 705
E--> 884 tgg ggc gac acg gtc gtc gac gtc ggc gag cgg agc ctg cgc gac gag
     885 2932
     886 Trp Gly Asp Thr Val Val Asp Val Gly Glu Arg Ser Leu Arg Asp Glu
     887 715
                           720
                                                 725
E--> 889 ctg acc ggc cgc gag gcc cgc gga gcg gcg cgc gtg gcc gag ttg ttc
     890 2980
     891 Leu Thr Gly Arg Glu Ala Arg Gly Ala Ala Arg Val Ala Glu Leu Phe
     892
                        735
                                             740
E--> 894 gcc gac tac ccc gtc gcc ctg ctg gtg gag aca tgaaccgacg attcccggtc
     895 3033
     896 Ala Asp Tyr Pro Val Ala Leu Leu Val Glu Thr
     897
                    750
                                         755
E--> 899 tgggcgcccc aggccgcgca ggtgacgctc gtcgtgggcc aaggccgcgc cgaactcccg
     900 3093
E--> 902 ctgacccgcg acgagaacgg atggtgggct cttcagcagc cgtgggacgg cggccccgac
     903 3153
E--> 905 ctcgtcgact acggctacct cgtcgacggc aagggcccct tcgccgaccc gcggtcgctg
     906 3213
E--> 908 cggcagccgc gcggcgtgca cgagctcggc cgcgaattc
     909 3252
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     915 <212> TYPE: DNA
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     918 <220> FEATURE:
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     923 26
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     931 <220> FEATURE:
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    936 25
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some

940 <211> LENGTH: 50

Input Set : A:\Yamamtol.app Output Set: N:\CRF3\03232001\I435770.raw 941 <212> TYPE: DNA 942 <213> ORGANISM: Artificial 'Sequence 944 <220> FEATURE: 945 <223> OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC 947 <400> SEQUENCE: 22 E--> 948 aattotttt taataaaato aggaggaato tagatgttta otagtotgoa 949 50 952 <210> SEQ ID NO: 23 953 <211> LENGTH: 42 954 <212> TYPE: DNA 955 <213> ORGANISM: Artificial Sequence 957 <220> FEATURE: 958 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC 960 <400> SEQUENCE: 23 E--> 961 gactagtaaa catctagatt cctcctgatt ttattaaaaa ag 962 42 965 <210> SEQ ID NO: 24 966 <211> LENGTH: 33 967 <212> TYPE: DNA 968 <213> ORGANISM: Artificial Sequence 970 <220> FEATURE: 971 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC 973 <400> SEQUENCE: 24 E--> 974 aaatctagat gcccgccagt acctaccgcc ttc 975 33 978 <210> SEQ ID NO: 25 979 <211> LENGTH: 33 980 <212> TYPE: DNA 981 <213> ORGANISM: Artificial Sequence 983 <220> FEATURE: 984 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC 986 <400> SEQUENCE: 25 E--> 987 aaaactagtt tatcatgtct ccaccagcag ggc 988 33 991 <210> SEQ ID NO: 26 992 <211> LENGTH: 22 993 <212> TYPE: DNA 994 <213> ORGANISM: Artificial Sequence 996 <220> FEATURE: 997 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC 999 <400> SEQUENCE: 26 E--> 1000 atcggtgatg tcggcgatat ag 1001 22 1004 <210> SEQ ID NO: 27 1005 <211> LENGTH: 29 1006 <212> TYPE: DNA 1007 <213> ORGANISM: Artificial Sequence 1009 <220> FEATURE: 1010 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/435,770

some

DATE: 03/23/2001

TIME: 16:39:39

Input Set : A:\Yamamtol.app Output Set: N:\CRF3\03232001\I435770.raw 1012 <400> SEQUENCE: 27 E--> 1013 gtactggcgg gcatattttt tcctcctga 1014 29 1017 <210> SEQ ID NO: 28 1018 <211> LENGTH: 31 1019 <212> TYPE: DNA 1020 <213> ORGANISM: Artificial Sequence 1022 <220> FEATURE: 1023 <223> OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC 1025 <400> SEQUENCE: 28 E--> 1026 aatcaggagg aaaaaatatg cccgccagta c 1027 31 1030 <210> SEQ ID NO: 29 1031 <211> LENGTH: 22 1032 <212> TYPE: DNA 1033 <213> ORGANISM: Artificial Sequence 1035 <220> FEATURE: 1036 <223> OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC 1038 <400> SEQUENCE: 29 same E--> 1039 tcgacgatct gggtgagcgg at 1040 22 1043 <210> SEQ ID NO: 30 1044 <211> LENGTH: 22 1045 <212> TYPE: DNA 1046 <213> ORGANISM: Artificial Sequence 1048 <220> FEATURE: 1049 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC 1051 <400> SEQUENCE: 30 E--> 1052 tcgacgagca cccggtcgat cc 1053 22 1056 <210> SEQ ID NO: 31 1057 <211> LENGTH: 26 1058 <212> TYPE: DNA 1059 <213> ORGANISM: Artificial Sequence 1061 <220> FEATURE: 1062 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC Free item 10 on Eva Sunnay Sheet 1064 <400> SEQUENCE: 31 E--> 1065 cartgggayg aygaygunga ycaygc 1066 26 1069 <210> SEQ ID NO: 32 1070 <211> LENGTH: 2218 1071 <212> TYPE: DNA 1072 <213> ORGANISM: Artificial Sequence 1074 <220> FEATURE: 1075 <223> OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC 1077 <220> FEATURE: 1078 <221> NAME/KEY: CDS 1079 <222> LOCATION: (477)..(2201) 1081 <220> FEATURE:

DATE: 03/23/2001

TIME: 16:39:39

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/435,770

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/435,770

DATE: 03/23/2001 TIME: 16:39:39

Input Set : A:\Yamamtol.app

Output Set: N:\CRF3\03232001\I435770.raw

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James James James

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/435,770

Input Set : A:\Yamamtol.app
Output Set: N:\CRF3\03232001\I435770.raw

E--> 1147 gga acg ctg gac agc gcc atc cgt cgc ctc gac cac ctg gtg cgc ctc 1148 863 1149 Gly Thr Leu Asp Ser Ala Ile Arg Arg Leu Asp His Leu Val Arg Leu 1150 115 120 125 E--> 1152 ggc gtc gac gcg gtc gag ctg ctg ccc gtc aac gcg ttc aac ggc acc 1153 911 1154 Gly Val Asp Ala Val Glu Leu Leu Pro Val Asn Ala Phe Asn Gly Thr 1155 130 135 140 E--> 1157 cac ggc tgg ggc tac gac ggg gtg ctc tgg tac gcg gtg cac gag ccc 1158 959 1159 His Gly Trp Gly Tyr Asp Gly Val Leu Trp Tyr Ala Val His Glu Pro 1160 150 155 E--> 1162 tac ggc ggc ccg gag gcg tac cag cgc ttc gtc gac gcc tgc cac gcc 1163 1007 1164 Tyr Gly Gly Pro Glu Ala Tyr Gln Arg Phe Val Asp Ala Cys His Ala 1165 165 170 E--> 1167 cgc ggc ctc gcc gtc gtg cag gac gtc gtc tac aac cac ctg ggc ccg 1168 1055 1169 Arg Gly Leu Ala Val Val Gln Asp Val Val Tyr Asn His Leu Gly Pro 1170 180 185 E--> 1172 age ggc aac cac etg eec gac tte gge eec tae etc ggg teg gge gee 1173 1103 1174 Ser Gly Asn His Leu Pro Asp Phe Gly Pro Tyr Leu Gly Ser Gly Ala 1175 195 205 200 E--> 1177 gcc aac acc tgg ggc gac gcg ctg aac ctc gac ggg ccg ctc tcc gac 1178 1151 1179 Ala Asn Thr Trp Gly Asp Ala Leu Asn Leu Asp Gly Pro Leu Ser Asp 1180 210 215 220 E--> 1182 gag gtg cgg cgg tac atc atc gac aac gcg gtg tac tgg ctg cgc gac 1183 1199 1184 Glu Val Arg Arg Tyr Ile Ile Asp Asn Ala Val Tyr Trp Leu Arg Asp 1185 230 235 E--> 1187 atg cac gcc gac ggg ctg cgg ctc gac gcc gtg cac gcg ctg cgc gac 1188 1247 1189 Met His Ala Asp Gly Leu Arg Leu Asp Ala Val His Ala Leu Arg Asp 1190 245 250 E--> 1192 gcc cgc gcg ctg cac ctg ctc gaa gag ctc gcc gcc cgc gtc gac gag 1194 Ala Arg Ala Leu His Leu Leu Glu Glu Leu Ala Ala Arg Val Asp Glu 1195 260 265 270 E--> 1197 ctg gcg ggc gag ctc ggc cgg ccg ctg acg ctc atc gcc gag agc gac 1198 1343 1199 Leu Ala Gly Glu Leu Gly Arg Pro Leu Thr Leu Ile Ala Glu Ser Asp 1200 275 280 285 E--> 1202 ctg aac gac ccg aag ctg atc cgc tcc cgc gcg gcg cac ggc tac ggc 1203 1391 1204 Leu Asn Asp Pro Lys Leu Ile Arg Ser Arg Ala Ala His Gly Tyr Gly 1205 290 295 300 E--> 1207 ctc gac gcc cag tgg gac gac gtg cac cac gcg gtg cac gcc aac

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DATE: 03/23/2001

TIME: 16:39:39

RAW SEQUENCE LISTING PATENT APPLICATION: US/09/435,770 DATE: 03/23/2001 TIME: 16:39:39

Input Set : A:\Yamamtol.app
Output Set: N:\CRF3\03232001\I435770.raw

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		Leu Asp	Δla	G1 n	Tro	Asn	Asp	Asn	Va 1	His	His	Ala	Va 1	His	Ala	Asn
	1210	Deu 115p		0	310			пор		315					320	
E>		gtg acc	aac	gag		qtc	aac	tac	tac		gac	ttc	qqc	aaa		aac
_		1487				•				•	•					
	1214	Val Thr	Gly	Glu	Thr	Val	Gly	Tyr	Tyr	Ala	Asp	Phe	Gly	Gly	Leu	Gly
	1215		_	325			-	•	330		-		_	335		_
E>	1217	gcc ctc	gtc	aag	gtg	ttc	cag	cgc	ggc	tgg	ttc	cac	gac	ggc	acc	tgg
	1218	1535														
		Ala Leu		Lys	Val	Phe	Gln	Arg	Gly	Trp	Phe	His	Asp	Gly	Thr	Trp
	1220		340					345					350			
E>		tcg agc	ttc	cgc	gag	cgg	cac	cac	ggc	cgg	ccg	ctc	gac	ccc	gac	atc
		1583	_													_
		Ser Ser	Phe	Arg	Glu	Arg		His	Gly	Arg	Pro		Asp	Pro	Asp	Ile
	1225	355					360					365				
E>		ccg ttc	cgc	cgg	CtC	gtc	gcc	ttc	gcg	cag	gat	cac	gac	cag	gtc	ggc
		1631 Pro Phe	3 ===	3	T 0.11	1701	7 l a	Dho	212	C15	3.00	ni o	1 an	Cln	Wa I	C1**
	1230		AIG	ALG	neu	375	нта	Pile	нта	GTII	380	пть	ASP	GIII	Val	385
F>		aac cga	aca	atc	aac		cac	atα	tca	aca		atc	aac	nan	aat	
- /		1679	909	9 00	990	gue	cyc	ucy	ccg	909	cug	900	990	949	990	209
		Asn Arg	Ala	Val	Glv	Asp	Arg	Met	Ser	Ala	Gln	Val	Glv	Glu	Glv	ser
	1235				390		5			395					400	
E>	1237	ctc gcc	gcc	gcg	gcg	gcg	ctc	gtg	ctg	ctc	ggc	ccg	ttc	acc	ccg	atg
		1727														
	1239	Leu Ala	Ala	Ala	Ala	Ala	Leu	Val	Leu	Leu	Gly	${\tt Pro}$	Phe	Thr	Pro	Met
	1240			405					410					415		
E>		ctg ttc	atg	ggc	gag	gag	tgg	ggc	gcg	cgc	acc	ccg	tgg	cag	ttc	ttc
		1775							_				_			
		Leu Phe		Gly	Glu	Glu	Trp	-	Ala	Arg	Thr	Pro	_	Gln	Phe	Phe
	1245		420					425					430			
F>		acc tcc 1823	Cac	CCC	yay	CCC	yay	CLG	999	yay	geg	acy	gcg	cgc	999	cgc
		Thr Ser	Hic	Pro	Glu	Pro	Glu	Leu	Glv	Glu	Δla	Thr	Ala	Ara	Glv	Arσ
	1250	435					440		1			445			J-1	
E>	1252	atc gcc	gag	ttc	gcc	cgc	atg	ggc	tgg	gac	ccg	gca	gtc	gtg	ccc	gac
		1871			-	-	-			_	_	-				
	1254	Ile Ala	Glu	Phe	Ala	Arg	Met	Gly	Trp	Asp	Pro	Ala	Val	Val	Pro	Asp
	1255					455					460					465
E>		ccg cag	gac	ccg	gcc	acc	ttc	gcc	cgc	tcg	cac	ctg	gac	tgg	tcc	gag
	_	1919														
		Pro Gln	Asp	Pro		Thr	Phe	Ala	Arg		His	Leu	Asp	Trp		Glu
	1260				470					475					480	
E>		ccc gag	cgg	gaa	ccg	cac	gcg	ggc	ctg	ctc	gcc	ttc	tac	acc	gac	ctg
	1263		7 ~~	C1	Dro	uia	71 -	c1	T 0	T 0"	A 1 -	Dho	тк∙∽	mb ∽	7.00	Lou
	1264	Pro Glu	ALG	485	PLO	птя	AId	сту	490	ьец	WIG	PHE	TAL	495	нар	пеп
E>		atc gcg	cte		cac	gag	cta	cca		gat	aca	cca	aca		αaα	ata
- /	1268		~ ~ ~	~99	-yc	349	~ -9	9	3	Juc	3~9	Jug	3~3	Jyc	3.73	3-3
	_200															

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Input Set : A:\Yamamtol.app

Output Set: N:\CRF3\03232001\I435770.raw

1269 Ile Ala Leu Arg Arg Glu Leu Pro Val Asp Ala Pro Ala Arg Glu Val 1270 500 505 510 E--> 1272 gat gcc gac gag gcg cgc ggc gtc ttc gcg ttc agc cgc ggc ccg ctg 1273 2063 1274 Asp Ala Asp Glu Ala Arg Gly Val Phe Ala Phe Ser Arg Gly Pro Leu 1275 515 520 525 E--> 1277 cgg gtc acg gtc gcg ctg cgc ccc gga ccg gtc ggg gtg ccc gag cac 1278 2111 1279 Arg Val Thr Val Ala Leu Arg Pro Gly Pro Val Gly Val Pro Glu His 1280 530 535 540 E--> 1282 ggg ggc ctc gtg ctc gcc tac ggc gag gtg cgc gcc ggc gcc gga 1283 2159 1284 Gly Gly Leu Val Leu Ala Tyr Gly Glu Val Arg Ala Gly Ala Ala Gly 1285 550 555 E--> 1287 ctg cac ctc gac ggg ccg gga gcc gcg atc gtg cgc ctc gag 1288 2201 1289 Leu His Leu Asp Gly Pro Gly Ala Ala Ile Val Arg Leu Glu 1290 565 570 E--> 1292 tgacgcggct gggtacc 1293 2218 1296 <210> SEQ ID NO: 33 1297 <211> LENGTH: 25 1298 <212> TYPE: DNA 1299 <213> ORGANISM: Artificial Sequence 1301 <220> FEATURE: 1302 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC 1304 <400> SEQUENCE: 33 E--> 1305 atgaaccgac gattcccggt ctggg 1306 25 1308 <210> SEQ ID NO: 34 1309 <211> LENGTH: 25 1310 <212> TYPE: DNA 1311 <213> ORGANISM: Artificial Sequence 1313 <220> FEATURE: 1314 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC 1316 <400> SEQUENCE: 34 E--> 1317 tcactcgagg cgcacgatcg cggct

same

1318 25

VERIFICATION SUMMARY DATE: 03/23/2001 PATENT APPLICATION: US/09/435,770 TIME: 16:39:40

Input Set : A:\Yamamtol.app

Output Set: N:\CRF3\03232001\I435770.raw

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L:247 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:7
M:254 Repeated in SeqNo=7
L:331 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:28 SEQ:8
L:535 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:17
M:254 Repeated in SeqNo=17
L:601 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:18
L:623 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:19
M:254 Repeated in SeqNo=19
L:922 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:26 SEQ:20
L:935 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:25 SEQ:21
L:948 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:22
L:961 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:42 SEQ:23
L:974 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:33 SEQ:24
L:987 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:33 SEQ:25
L:1000 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:26
L:1013 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:29 SEQ:27
L:1026 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:31 SEQ:28
L:1039 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:29
L:1052 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:30
L:1065\ M:258\ W: Mandatory Feature missing, <221> not found for SEQ ID#:31
L:1065 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:31
L:1065 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:31
L:1065 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:26 SEQ:31
L:1085 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:32 differs:33
L:1086 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:32
M:254 Repeated in SeqNo=32
L:1305 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:25 SEQ:33 L:1317 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:25 SEQ:34
L:1330 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:36 SEQ:35
L:1343 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:36 SEQ:36
L:1356 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:28 SEQ:37
L:1369 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:28 SEQ:38 L:1382 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:39
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